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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/785,548
DATE: 11/14/2001
TIME: 09:59:45

Input Set : A:\st0005seq.txt
Output Set: N:\CRF3\11142001\I785548.raw

3 <110> APPLICANT: AVENTIS PHARMACEUTICALS, INC.
6 <120> TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF
PARKIN
9 <130> FILE REFERENCE: ST00005
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/785,548 OK
C--> 12 <141> CURRENT FILING DATE: 2001-02-20 OK

14 <160> NUMBER OF SEQ ID NOS: 46
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1313
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(1032)
27 <400> SEQUENCE: 1

ENTERED

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29	Gln Asn Leu Pro Ser Ser Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly	
30	1 5 10 15	
32	ttt aga cac gga agt tta att agc att gac agc acc tgt aca gag atg	96
33	Phe Arg His Gly Ser Leu Ile Ser Ile Asp Ser Thr Cys Thr Glu Met	
34	20 25 30	
36	ggc aat ttt gac aat gct aat gtc act gga gaa ata gaa ttt gcc att	144
37	Gly Asn Phe Asp Asn Ala Asn Val Thr Gly Glu Ile Glu Phe Ala Ile	
38	35 40 45	
40	cat tat tgc ttc aaa acc cat tct tta gaa ata tgc atc aag gcc tgt	192
41	His Tyr Cys Phe Lys Thr His Ser Leu Glu Ile Cys Ile Lys Ala Cys	
42	50 55 60	
44	aag aac ctt gcc tat gga gaa gaa aag aag aaa aag tgc aat ccg tat	240
45	Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr	
46	65 70 75 80	
48	gtg aag acc tac ctg ttg ccc gac aga tcc tcc cag gga aag cgc aag	288
49	Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys	
50	85 90 95	
52	act gga gtc caa agg aac acc gtg gac ccg acc ttt cag gag acc ttg	336
53	Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr Leu	
54	100 105 110	
56	aag tat cag gtg gcc cct gcc cag ctg gtg acc cgg cag ctg cag gtc	384
57	Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln Val	
58	115 120 125	
60	tcg gtg tgg cat ctg ggc acg ctg gcc cgg aga gtg ttt ctt gga gaa	432
61	Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly Glu	
62	130 135 140	
64	gtg atc att tct ctg gcc acg tgg gac ttt gaa gac agc aca aca cag	480
65	Val Ile Ile Ser Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln	
66	145 150 155 160	
68	tcc ttc cgc tgg cat ccg ctc cgg gcc aag gcg gag aaa tac gaa gac	528
69	Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp	

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70          165          170          175
72 agc gtt cct cag agt aat gga gag ctc aca gtc cgg gct aag ctg gtt 576
73 Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu Val
74          180          185          190
76 ctc cct tca cgg ccc aga aaa ctc caa gag gct caa gaa ggg aca gat 624
77 Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp
78          195          200          205
80 cag cca tca ctt cat ggt caa ctt tgt ttg gta gtg cta gga gcc aag 672
81 Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala Lys
82          210          215          220
84 aat tta cct gtg cgg cca gat ggc acc ttg aac tca ttt gtt aag ggc 720
85 Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys Gly
86 225          230          235          240
88 tgt ctc act ctg cca gac caa caa aaa ctg aga ctg aag tcg cca gtc 768
89 Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro Val
90          245          250          255
92 ctg agg aag cag gct tgc ccc cag tgg aaa cac tca ttt gtc ttc agt 816
93 Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe Ser
94          260          265          270
96 ggc gta acc cca gct cag ctg agg cag tcg agc ttg gag tta act gtc 864
97 Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr Val
98          275          280          285
100 tgg gat cag gcc ctc ttt gga atg aat gac cgc ttg ctt gga gga acc 912
101 Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly Thr
102          290          295          300
104 aga ctt ggt tca aag gga gac aca gct gtt ggc ggg gat gca tgc tca 960
105 Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys Ser
106 305          310          315          320
108 cta tcg aag ctc cag tgg cag aaa gtc ctt tcc agc ccc aat cta tgg 1008
109 Leu Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu Trp
110          325          330          335
112 aca gac atg act ctt gtc ctg cac tgacatgaag gcctcaaggt tccaggttgc 1062
113 Thr Asp Met Thr Leu Val Leu His
114          340
116 agcaggcgtg aggcactgtg cgtctgcaga ggggctacga accaggtgca ggggtcccagc 1122
118 tggagacccc tttgaccttg agcagtcctc atctgcggcc ctgtcccatg gcttaaccgc 1182
120 ctattggtat ctgtgtatat ttacgttaaa cacaattatg ttacctaagc ctctggtggg 1242
122 ttatctcctc tttgagatgt agaaaatggc cagattttaa taaacgttgt tacccatgaa 1302
124 aaaaaaaaaa a 1313
127 <210> SEQ ID NO: 2
128 <211> LENGTH: 344
129 <212> TYPE: PRT
130 <213> ORGANISM: Homo sapiens
132 <400> SEQUENCE: 2
133 Gln Asn Leu Pro Ser Ser Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly
134 1 5 10 15
136 Phe Arg His Gly Ser Leu Ile Ser Ile Asp Ser Thr Cys Thr Glu Met
137 20 25 30
139 Gly Asn Phe Asp Asn Ala Asn Val Thr Gly Glu Ile Glu Phe Ala Ile

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140          35          40          45
142 His Tyr Cys Phe Lys Thr His Ser Leu Glu Ile Cys Ile Lys Ala Cys
143          50          55          60
145 Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr
146 65          70          75          80
148 Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys
149          85          90          95
151 Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr Leu
152          100          105          110
154 Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln Val
155          115          120          125
157 Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly Glu
158          130          135          140
160 Val Ile Ile Ser Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln
161 145          150          155          160
163 Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp
164          165          170          175
166 Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu Val
167          180          185          190
169 Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp
170          195          200          205
172 Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala Lys
173          210          215          220
175 Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys Gly
176 225          230          235          240
178 Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro Val
179          245          250          255
181 Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe Ser
182          260          265          270
184 Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr Val
185          275          280          285
187 Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly Thr
188          290          295          300
190 Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys Ser
191 305          310          315          320
193 Leu Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu Trp
194          325          330          335
196 Thr Asp Met Thr Leu Val Leu His
197          340
201 <210> SEQ ID NO: 3
202 <211> LENGTH: 471
203 <212> TYPE: DNA
204 <213> ORGANISM: Homo sapiens
206 <220> FEATURE:
207 <221> NAME/KEY: CDS
208 <222> LOCATION: (1)..(471)
210 <400> SEQUENCE: 3
211 gga agt cca gca ggt aga tca atc tac aac agc ttt tat gtg tat tgc 48
212 Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn Ser Phe Tyr Val Tyr Cys

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213      1              5              10              15
215 aaa ggc ccc tgt caa aga gtg cag ccg gga aaa ctc agg gta cag tgc      96
216 Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln Cys
217              20              25              30
219 agc acc tgc agg cag gca acg ctc acc ttg acc cag ggt cca tct tgc      144
220 Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu Thr Gln Gly Pro Ser Cys
221              35              40              45
223 tgg gat gat gtt tta att cca aac cgg atg agt ggt gaa tgc caa tcc      192
224 Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser
225              50              55              60
227 cca cac tgc cct ggg act agt gca gaa ttt ttc ttt aaa tgt gga gca      240
228 Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly Ala
229      65              70              75              80
231 cac ccc acc tct gac aag gaa aca tca gta gct ttg cac ctg atc gca      288
232 His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile Ala
233              85              90              95
235 aca aat agt cgg aac atc act tgc att acg tgc aca gac gtc agg agc      336
236 Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg Ser
237              100              105              110
239 ccc gtc ctg gtt ttc cag tgc aac tcc cgc cac gtg att tgc tta gac      384
240 Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu Asp
241              115              120              125
243 tgt ttc cac tta tac tgt gtg aca aga ctc aat gat cgg cag ttt gtt      432
244 Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val
245      130              135              140
247 cac gac cct caa ctt ggc tac tcc ctg cct tgt gtg tag      471
248 His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val
249 145              150              155
252 <210> SEQ ID NO: 4
253 <211> LENGTH: 156
254 <212> TYPE: PRT
255 <213> ORGANISM: Homo sapiens
257 <400> SEQUENCE: 4
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259      1              5              10              15
260 Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln Cys
261              20              25              30
262 Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu Thr Gln Gly Pro Ser Cys
263              35              40              45
264 Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser
265              50              55              60
266 Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly Ala
267      65              70              75              80
268 His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile Ala
269              85              90              95
270 Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg Ser
271              100              105              110
272 Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu Asp
273              115              120              125

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274 Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val
275      130                      135                      140
276 His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val
277 145                      150                      155
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282 <211> LENGTH: 27
283 <212> TYPE: DNA
284 <213> ORGANISM: Artificial sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Description of the artificial sequence:Oligonucleotide
289 <400> SEQUENCE: 5
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293 <210> SEQ ID NO: 6
294 <211> LENGTH: 29
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: Description of the artificial sequence:Oligonucleotide
301 <400> SEQUENCE: 6
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305 <210> SEQ ID NO: 7
306 <211> LENGTH: 19
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Description of the artificial sequence:Oligonucleotide
313 <400> SEQUENCE: 7
314 gcgtttggaa tcactacag                      19
317 <210> SEQ ID NO: 8
318 <211> LENGTH: 17
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: Description of the artificial sequence:Oligonucleotide
325 <400> SEQUENCE: 8
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329 <210> SEQ ID NO: 9
330 <211> LENGTH: 18
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial sequence
334 <220> FEATURE:
335 <223> OTHER INFORMATION: Description of the artificial sequence:Oligonucleotide
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341 <210> SEQ ID NO: 10
342 <211> LENGTH: 18
343 <212> TYPE: DNA
344 <213> ORGANISM: Artificial sequence
346 <220> FEATURE:

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/785,548

DATE: 11/14/2001

TIME: 09:59:46

Input Set : A:\st0005seq.txt

Output Set: N:\CRF3\11142001\I785548.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date